

Journal of Molecular Biology, 1999, 294, 489-500

DOI: 10.1006/jmbo.1999.1122 Article ID: 00001122

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Journal of Molecular Biology, 1999, 294, 489-500

BioMedNet

DOMO: a new database of aligned protein domains

John A. Gray and Karen K. Argos
Trends in Biochemical Sciences, 1998, **23**, 486-487

Abstract

There is no abstract for this article. The text below is the first paragraph of text within the article.

Comparing aligned protein domains can help us to understand protein function. However, aligning domains from different proteins is difficult due to multiple sequence alignment, domain detection, and the lack of a consensus sequence determination of each domain. In addition, domain databases do not exist for all proteins. Consequently, although many multiple-domain databases (e.g., PDB, ProDom) exist, as yet there are no full domain alignment databases. PRODOM and PRODIST have been constructed to analyze automated prokaryotic sequence alignments and to

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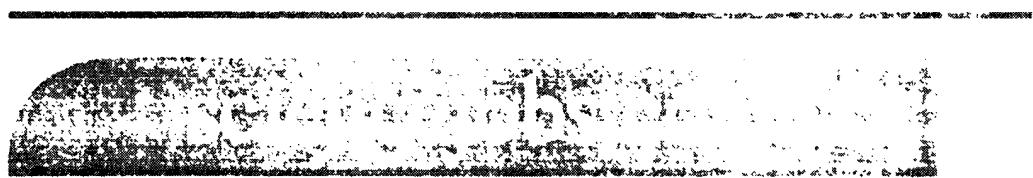
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